Amendments to the Specification:

Please replace the paragraph beginning at page 16, line 1 with the following amended paragraph:

"Homologues" of the MUC1-binding members described herein may be formed by substitution, addition, or deletion of one or more amino acids employing methods well known in the art and for particular purposes known in the art. Such "homologous" proteins, polypeptides, or peptides will be understood to fall within the scope of the present invention so long as the substitution, addition, or deletion of amino acids does not eliminate its ability to bind MUC1 or to form part of a MUC1 binding domain. The term "homologous", as used herein, refers to the degree of sequence similarity between two polymers (i.e., polypeptide molecules or nucleic acid molecules). When the same nucleotide or amino acid residue occupies a sequence position in the two polymers under comparison, then the polymers are homologous at that position. For example, if the amino acid residues at 60 of 100 amino acid positions in two polypeptide sequences match or "are homologous", then the two sequences are 60% homologous. The homology percentage figures referred to herein reflect the maximal homology possible between the two polymers, i.e., the percent homology when the two polymers are so aligned as to have the greatest number of matched (homologous) positions. Various computer programs are available for aligning two polymers and also for calculating the percent homology between the two polymers. For example, alignment and/or percent homology calculations between two polymers of interest are routinely performed using the BLAST sequence bank computer program (see, e.g., ~~http://~~www.ncbi.nlm.nih.gov/blast/) or the MCVECTOR® computer program. For germ line homology studies, Vbase (see, e.g., ~~http://~~www.mrc-cpe.cam.ac.uk/imt-doc/) performs alignments between new and known germ line sequences in order to determine the source of individual $V_L$ or $V_H$ regions of an antibody molecule. Protein, polypeptide, and peptide homologues within the scope of the present invention will be about 70%, preferably about 80%, and more preferably about 90% or more (including about 95%, about 97%, or even about 99% or more) homologous to a MUC1-binding member, a MUC1 binding domain, or portion thereof,

including a CDR or a CDR and selected contiguous framework (FR) residues, as disclosed herein. Polynucleotide homologues within the scope of the present invention will be about 60%, preferably about 70%, more preferably about 80%, and even more preferably about 90% or more (including about 95%, about 97%, or even about 99% or more) homologous to the nucleotide sequences described herein that encode a MUC1-specific binding member, a MUC1 binding domain, or portion thereof (such as $V_L$, $V_H$, CDR), as disclosed herein.

Please replace the paragraph beginning at page 33, line 16 with the following amended paragraph:

Screening and characterization of cell binding clones by whole cell ELISA, fingerprint analysis, flow cytometry, sequencing, indirect epitope fingerprinting and immunohistochemistry was performed according to the methods we described before (Hoogenboom et al., *Eur. J. Biochem., 260*: 774-84 (1999), Henderikx et al., *Cancer Res., 58*: 4324-32 (1998)). For screening purposes, individual clones were picked and transferred to 96-well plate and phage was produced as described in (Marks et al., *J. Mol. Biol., 222*: 581-597 (1991)). Individual clones of rounds 4 and 5 were tested for their specificity by whole cell ELISA (Hoogenboom et al., *Eur. J Biochem., 260*: 774-84 (1999)) on a MUC1-negative murine fibroblast cell line 3T3 and a MUC1-transfected 3T3 cell line. Clones were considered positive in whole cell ELISA when the $A_{450}$ (horseradish peroxidase staining reaction) of the MUC1-transfected 3T3 cell line was at least 3 times higher than the $A_{450}$ of the MUC1-negative 3T3 cell line. Positive clones were screened for diversity in fingerprint analysis by polymerase chain reaction (PCR), using primer CHIFOR (5'-GTC CTT GAC CAG GCA GCC CAG GGC-3') (SEQ ID NO:9), from the constant CH1 region of Fab antibodies, and pUC-reverse (5'-AGC GGA TAA CAA TTT CAC ACA GG-3') (SEQ ID NO:10), followed by *Bst*NI enzyme digestion and analysis of the restriction fragments by agarose gel electrophoresis (Marks et al., *J. Mol. Biol., 222*: 581-597 (1991), Gussow et al., *Nucleic Acids Res., 17*: 4000 (1989)). Cell binding of unique positive clones was evaluated by flow cytometric analysis of phage binding pattern (Rousch et al., *Br. J. Pharmacol., 125*: 5-16 (1998)) on the same cell lines as used during the selection. The V-genes

of one Fab, clone PH1, were sequenced using a cycle sequencing kit according to the directions of the manufacturer (Edge Biosystems, Gaithersburg, Md.). Primers were the same as for fingerprinting. Nucleotide sequences and their corresponding deduced amino acid sequences were aligned and compared to the germ line sequences of the Sanger Center Sequence database (~~http://~~www.sanger.ac.uk/DataSearch/gq_search.shtml) (Table 2). As shown in Table 2, the $V_H$ region of the PH1 Fab antibody is a $V_H$ region from the DP47 germ line, and the $V_L$ region is a $V_L$ region from the DPK15 germ line. The selection strategies used here are compared with selections on MUC1 that were previously described (see, Table 1; de Haard et al., *J. Biol. Chem.*, *274*: 18218-18230 (1999), Henderikx et al., *Cancer Res.*, *58*: 4324-32 (1998)). Likewise, the further characterization of the clones and constructs was performed by methods previously described (see, Henderikx et al., *Cancer Res.*, *58*: 4324-32 (1998)) and are specified only briefly herein.